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Title:
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Maximum
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
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                                                                                                  of hits satisfying chosen parameters:
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Match
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286
1 RALCTICSDFFDHSRI
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Listing first 45 summaries
   BLOSUM62
Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
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 RNF4_HUMAN
RNF4_RAT
A33_PLEWA
RAFS_TORGA
CBLC_HUMAN
YQO9_CAEEL
RRAPS_CHICK
MKR3_MOUSE
RAPS_HUMAN
RAPS_HOUSE
BMI1_HUMAN
RAPS_CAEEL
BMI1_HUMAN
MKR4_HUMAN
MK74_HUMAN
YP99_CAEEL
BMI1_HUMAN
MK74_HUMAN
YP99_CAEEL
Z173_HUMAN
YP99_CAEEL
Z173_HUMAN
XT19_HUMAN
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XT19_HUMAN
XT19_HUMAN
XT18_CAEEL
Z172_HUMAN
XTLB5_CAEEL
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O4003 drosophila
P25916 mus musculu
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O9477 caenorhabdi
O12899 homo sapien
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Best Local
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16-OCT-2001 (Rel. 40, 0
16-OCT-2001 (Rel. 40, 0
16-OCT-2001 (Rel. 40, 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     critical region.";
Dev. Dyn. 218:102-111(2000).
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MEDLINE-20284895;
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Transcription regulation; Activator; Zinc-finger; Nuclear ZN_FING 132 177 RING-TYPE.
SEQUENCE 190 AA; 21319 MW; E5E3AE4A9B28CF9D CRC64;
(RNF4)
               Fusco A., Bruni C.B.
"Identification and
                                                  MEDLINE=98140125; PubMed=9479498;
Chiariotti L., Benvenuto G., Fedele
                                                                                          TISSUE=Embryo
                                                                                                            SEQUENCE OF 16-178
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                        "Functional annotation of Nature 409:685-690(2001).
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4895; PubMed=10822263;
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8; Mismatches
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             RING-finger gene
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OC RUKK
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OC EUKK
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R EMBL; BC003282; AAHU3202...

JR EMBL; U95141; AAC53539.1; -.

JR EMBL; U95141; AAC53539.1; -.

JR MGD; MGI:1201691; Rnf4.

DR Interpro; IPR001641; Znf_ring.

DR Pfam; PF00097; Zf-C3HC4; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS000518; ZF_RING_1; 1.

DR PROSITE; PS00089; ZF_RING_2; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

Transcription regulation; Activator; Zinc-finger; Nuclear protein.

KW Transcription 136 181 RING-TYPE.

KW TRING 136 181 RING-TYPE.
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Best Local
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                                                                                                                  "Identification of a novel RING finger protein as steroid receptor-mediated gene transcription."; Mol. Cell. Biol. 18:5128-5139(198).
-i- FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Porvervota: Metazoa; Chordata;
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Moilanen A.-M., Poukka H., Karvon
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                        ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION SUBUNIT: INTERACTS WITH GSCL, ANDROGEN RECEPTOR AND SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST 1.5
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DEVELOPING NERVOUS SYSTEM WITH STRONG EXPRESSION IN THE DOR
ROOT GANGLIA AND GONADS. UBIQUITOUSLY EXPRESSED IN THE ADUL
DEVELOPMENTAL STAGE: EXPRESSION IS DETECTED FROM EMBRYONIC
AND CONTINUES THROUGHOUT DEVELOPMENT AND INTO ADULTHOOD.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPICMDGYSEIVQNGRLIVSTECGHVFCSQCLRDSLKNA--NTCPTCRKKI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTIC----SDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF169300; AAF00620.1; -. AK019171; BAB31585.1; -. BC003282; AAH03282.1; -.
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(Rel. 40,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein 4 (SNURF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 1;
Pred. No. 7.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                           Craniata;
                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi;
                      ear and cytoplasmic EXPRESSED WITH HIG
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                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                         Hakli M.,
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                                                                                                 TRANSCRIPTION
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Q02084;
Q1-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR001841; Znf_ring.
Pf4m; PF00097; zf-C3H04; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Activator; ZN_FING 136 181 RING-TYPE SEQUENCE 194 AA; 21896 MW; 40C139
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93154311; PubMed=7679068; Bellini M., Lacroix J.-C., Gall J.G.; Putative zinc-binding protein on lampbrush chromosome loops."; PA putative zinc-binding protein on lampbrush chromosome loops."; EMBO J. 12:107-114(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 EMBL; L04190; AAA49614.1;
                                                             use by non-profit institutions as long modified and this statement is not removed
                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pleurodeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pleurodeles waltlii (Iberian ribbed newt).
Eukaryota; Metazoa; Chordata; Craniata; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-binding protein A33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                               tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                                                                                                                                                                 DEVELOPMENTAL STAGE: IT FIRST APPEARS ON THE CHROMOSOME LOOPS AND IN THE UCCLEOPLASM OF THE EGRAVINAL VESICLE (GV). IT IS TRANSMITTED TO THE EGG AT GV BEREAKDOWN AND APPEARS IN EMBRYONI NUCLEI AT THE MID-BLASTULA STAGE AND IS FOUND IN MANY BUT NOT ALL NUCLEI AT STILL LATER STAGES OF EMBRYOGENESIS.

SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

SIMILARITY: CONTAINS 1 BOX-TYPE ZINC FINGER.

SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear. DEVELOPMENTAL STAGE: IT FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                     IN THE GERMINAL VESICLE FOR USE DURING EARLY EMBRYOGENESIS AND MAY PLAY A ROLE IN THE SYNTHESIS OR PROCESSING OF PRE-
                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MAY BE A NUCLEAR REGULATORY PROTEIN THAT IS STORED
                                                                                                                                                                                                                                                                                                                          DURING OOGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPICMDGYSETVQNGRLIVSTECGHVFCSQCLRDSLKNA--NTCPTCRKKI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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37.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93; DB
Pred. No. 7.66
8; Mismatches
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; 40C13970FC11DFF2
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                                                                 Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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BUT NOT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                           RAPS_TORCA
P09108;
01-MAR-1989
                                                                   Carr C., McCourt D., Cohen J.B.;
"The 43-kilodalton protein of Torpedo nicomembranes: purification and determination Biochemistry 26:7090-7102(1987).
                                                                                                        SEQUENCE OF 8-412.
MEDLINE=88107644; PubMed=3427060;
Carr C., McCourt D., Cohen J.B.;
                                                                                                                                                                                                                                                   Torpedo californica (Pacific electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
43 kDa receptor-associated protein of the synapse (RAPSYN)
(Acetylcholine receptor-associated 43 kDa protein) (43 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
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ZN_FING
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                                                                                                                                                       Frail D.E., Mudd J., Shah V., Carr C., Cohen J.B., Mer "CDNAs for the postsynaptic 43 * NDa protein of Torpedo encode two proteins with different carboxyl termini.", proc. Natl. Acad. Sci. U.S.A. 84:6302-6306(1987).
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PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                       MEDLINE=88331095; PubMed=3417776; Musil L.S., Carr C., Cohen J.B.,
                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=87317641; PubMed=3476945;
                                                                                                                                                                                                                                          Torpediniformes; NCBI_TaxID=7787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc-finger;
RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003878;
InterPro; IPR000315;
"Acetylcholine receptor-associated bound myristate.";
                                                MYRISTOYLATION
                                                                                                                                                                                                                                                                                                       RAPSN
                                                                                                                                                                                                                                                                                                                postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00622; SPRY; 1.
PF000643; zf-B_box; 1.
PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SM00502; BBC; 1.
; SM00336; BBOX; 1.
; SM00184; RING; 1.
; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001870;
IPR003877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003649;
                                                                                                                                                                                                                                                                                                                                                   (Rel. 10, Created)
(Rel. 15, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                  protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein; Developmental protein; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
149
202
269
386
619
71056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BBOXZNFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%;
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Znf_bbox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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B BOX-TYPE.
COILED COIL.
SPRY.
60DBD1F3F071EFFD (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5; D
Pred. No. 0.00
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                       Merlie
             43K
                                                                                                                                                                                                                                                                                                                                                                                                    411
                                                                                  nicotinic posts
tion of primary
           protein
                       J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                    AΑ
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             contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                  postsynaptic
imary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                          Merlie J.P.;
                                                                                                                                                                               electric
            covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                    Q9ULVB; Q9Y5Z3; Q9Y5Z2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Signal transduction protein CBL-C (SH3-bind
CBLC OR CBL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
PROSITE;
PROSITE;
    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                 Homo sapiens (Human)
                                                                                                                                                                                                                   CBLC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS: PRO0217; POSTSYNAPTIC.
ProDom; PD012428; Postsynaptic; 1.
SMART; SM000184; RING; 1.
SMART; SM00028; TPR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001237; Postsynaptic.
InterPro; IPR001440; TPR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00515; TPR; 5.
Pfam; PF00097; Zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J02952; AAA49282.1; -. EMBL; J02953; AAA49283.1; -. PIR; A28009; A28009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synapse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myristate;
                                                                                                                                                                                                                                                                                                                                        362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXPRESSED, WHICH DIFFER IN THEIR C-TERMINUS.

DOMAIN: A CYSTEINE-RICH RECION HOMOLOGOUS TO ART OF THE
REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
SIMILARITY: BELONGS TO THE RAPSYN FAMILY.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell Biol. 107:1113-1121(1988).

FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.

SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO
                                                                                                                                                                                                                                                                                                                                      | CGLCGESIGDQNSQLQALPCSHLFHLKCL----QTNGNRGCPNCK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00405; 43_KD_POSTSYNAPTIC;
PS00518; ZF_RING_1; FALSE_NEC
PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Postsynaptic membrane; Cytoskeleton; Phosphorylation; e; Zinc-finger; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
195
404
389
361
393
410
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                              STANDARD;
  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
195
404
411
361
393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
MISSING (IN SHORT ISOFORM).
Y -> T (IN REF. 2).
N -> D (IN REF. 2).
Y -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RING-TYPE.
  Craniata; Ve Catarrhini;
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4D26262679FC9B4D CRC64;
                                                                                             cion update)
(SH3-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                           Vertebrata;
                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .00058;
  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                             protein CBL-C) (CBL-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISTINCT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
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DI DI AC

YOO9\_CAEEL QO9298; Q1-NOV-1997 Q1-NOV-1997 16-OCT-2001

Hypothetical

(Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
1 141.2 kDa protein EEED8.9 in chromosome

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CAEEL

STANDARD;

1238 A

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RESULT
YQO9_C/
                                                               В
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                                                                                                                                                                                                             Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                       Pfam; PF02262; Cbl_N; 1.
Pfam; PF02761; Cbl_N2; 1.
Pfam; PF02761; Cbl_N3; 1.
Pfam; PF00796; Cbl_N3; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                           VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB028645; BAA86298.1; -. EMBL; AF117646; AAD34341.1; -. EMBL; AF117647; AAD34342.1; -. HSSP; P22681; 1B47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 18:3365-3375(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: REGULATOR OF EGFR MEDIATED SIGNAL TRANSDUCTION.
-!- SUBUNIT: INTERACTS WITH A RESTRICTED RANGE OF SH3 DOMAIN PROTEINS.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene
                                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                         PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003153; Cbl_N.
InterPro; IPR000980; SH2.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: UBICUITOUS.
-!- PTM: PHOSPHORYLATED ON TYROSINES BY EGFR.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Pancreatic adenocarcinoma; MEDLINE-99289203; pubMed=10362357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20035821; PubMed=10571044;
Kim M., Tezuka T., Suzuki Y., Sugano S., Hirai M., Yamamoto T.;
"Molecular cloning and characterization of a novel cbl-family gene,
                                                                                                                                                                                                                                                                                          Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penninger J., Lipkowitz S.; "cbl-3: a new mammalian cbl family protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keane M.M., Ettenberg S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                               350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                            3 LCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
                                                              LCKICA---ESNKDVKIEPCGHLL-CSCCLAAWQHSDSQTCPFCRCEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239:145-154(1999).
                                                                                                                               16;
                                                                                                                              Similarity 33...
16; Conservative
                                                                                                                                                                                                                                                                         protein; Zinc-finger; Phosphorylation; Alternative 89 92 NUCLEAR LOCALIZATION SIGNAL (F
                                                                                                                                                                                                             AA;
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                                                                                                                                                                                                         390
306
1
234
52468 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LONG FORM)
                                                                                                                                             30.1%;
33.3%;
                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nau M.M., Banerjee P.,
                                                                                                                            Score 86; DB 1;
Pred. No. 0.0014;
2; Mismatches
                                                                                                                                                                                                                          RING-TYPE.
MISSING (IN SHORT ISOFORM).
T -> N (IN REF. 2).
                                                                                                                                                                                                           -> N (IN REF. 2).
91013DDF12828242 CRC64;
                                                                                                                               16;
                                                                                                                                                          Length 474
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuello
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RAPSCLT RAPSCLT ID SCR RAPSCLT ID SCR RAPSCLT ID SCR RAPSCLT IT SC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wormbep; EEED8.9; CE01893.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001841; Znf_ring.
InterPro; IPR001847; Zf-UBP.
Pfam; PF00069; pkinase; 2.
Pfam; PF00069; pkinase; 2.
Pfam; PF00148; zf-UBP; 1.
SMART; SM00184; RING; 1.
SMART; SM00290; Znf_UBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Z
ZN_FINC 908 945
DOMAIN 748 751
DOMAIN 124 1229
DOMAIN 1235 1238
SEQUENCE 1238 AA; 14
                                                                                                                                                                                                                                                                                                                                                                                                                    RAPS_CHICK
042393;
                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence
16-OCT-2001 (Rel. 40, Last annotati
43 kDa receptor-associated protein
(Acetylcholine receptor-associated
postsynaptic protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases -- SIMILARITY: TO YEAST YHLO10C AND S.POMBE SPAC16E8.1 -- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Burns A.L., Benson D., Howard M.J., Marg
"Chick ciliary ganglion neurons contain
                                             MEDLINE-97331014; PubMed-9185539;
                                                                                             SEQUENCE
                                                                                                                                                                                    Archosauria;
                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U23484; AAC46769.1; -.
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAVCLERMDDS--VLAILCNHSFHARCL----EQWADNTCPVCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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PS00518; ZF_RING_1; FALSE_NEG.
PS50089; ZF_RING_2; 1.
                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                       Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              945
751
1229
1238
                                                                                                                                                                                    Neognathae;
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                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger.
RING-TYPE.
FOLY-SER.
POLY-SER.
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                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
protein of the synapse (RAPSYN)
sociated 43 kDa protein) (43 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 86; DB Pred. No. 0.00 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-LYS.
WW; 5B9A6E03AF91A703
                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                     M.J., Margiotta
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            411
  transcripts
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0.0035;
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coding
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                                                                                                                                                                                  Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
  for
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001237; Postsynaptic.
InterPro; IPR001440; TPR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00515; TPR; 6.
PRINTS; PR00217; POSTSYNAPTIC.
PRODOM; PD012428; POSTSYNAPTIC: 1.
SMART; SM00184; RING; 1.
SMART; SM00184; TPR; 5.
                                                                                                                                                                    Q60764;
Q1-MAR-2002 (Rel. 41, Created)
Q1-MAR-2002 (Rel. 41, Last sequer
Q1-MAR-2002 (Rel. 41, Last annota
Makorin 3 (Zinc-finger protein 1:
MKRN3 OR ZFP127 OR ZNF127.
Jong M.T.C., Carey A.H., Caldwell K.A., Lau M.H., Handel M.A., Driscoll D.J., Stewart C.L., Rinchik E.M., Nicholls R.D.; "Imprinting of a RING zinc-finger encoding gene in the mouse chromosome region homologous to the Prader-Willi syndrome genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INIT_MET
ZN_FING
LIPID
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J. Neurosci. 17:5016-5026(1997).
-i- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
                                                           SEQUENCE FROM N. PubMed=10196368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Synapse: Postsynaptic membrane; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myristate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF000138; AAB63149.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                 MKR3_MOUSE
                                                                                                                                                                                                                                                                                                                                            362
                                                                                                                                                                                                                                                                                                                                                            4 CTICSDFF-DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: EXPRESSED IN MUSCLE FIBERS AND IN NEUF DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE REGULATORY DOMAIN OF PROTEIN KINES C MAY BE IMPORTANT IN INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER. SIMILARITY: BELONGS TO THE RAPSYN FAMILY. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                           CGMCGESIGEKNNQLQALPCSHFFHLKCL----QTNGTRGCPNCR
                                                                                                                                                                                                                                                                                                                                                                                                         . Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger.
0 0
362 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                1. 41, Createu,
1. 41, Last sequence upda
1. 41, Last annotation u
1. 7 protein 127).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195
                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46677
                                                                                                                                                                                                                                                                                                                                                                                                                      29
35.
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Pred. No. 0.00
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
RING-TYPE.
MYRISTATE (BY SIMILARITY).
PHOSPHORYLATION (POTENTIAL);
851E7B2F4645B459 CRC64;
                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                         Euteleostomi;
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Best Local S
Matches 18
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; Zf-C3HC4; 1.
Pfam; PF00642; Zf-CCCH; 3.
SMART; SM00184; RING; 1.
SMART; SM00186; ZnF_C3H1; 3.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS00518; ZF_RING_2; 1.
                                                  Buckel A., Beeson D., James M., Vincent A.;

Buckel A., Beeson D., James M., Vincent A.;

"Cloning of cDNA encoding human rapsyn and mapping of the RAPSN gene locus to chromosome 11p11.2-p11.1.";

Genomics 35:613-616(1996).

-i- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
                                                                                                                                                                                                                                                                                                                                                    RAPS_HUMAN STANDARD; PRT; 411 AA. 013702; 011-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 43 kDa receptor-associated protein of the synapse (Acetylcholine receptor-associated 43 kDa protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hum.
                                                                                                                                                                                                TISSUE-Muscle;
MEDLINE-97001170; PubMed-8812503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZN_FING
ZN_FING
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                               RAPSN
                                                                                                                                                                                                                                                                                                                                          postsynaptic protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 VCGICMEVVYEKADPTDRRFGILFSCNHTYCLRCIRRWRSATQFENRISKSCPQCRVSSG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LCTICSDFFDHSRDVA-----AMDCGHTFHLQCL----IQSFETAPSRTCPQCRIQVG 51
DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE INTERACTIONS OF THIS PROTEIN WITH THE LIPID I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . MO1. Genet. 8:795-803(1999).
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 3 C3H1-TYPE ZINC FINGERS.
                                                 MEMBRANES
                                                                                                                                                                                                                                                                                      sapiens (Human).

"atazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:99158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U19106; AAA76863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Repeat.
98 1
280 2
302 3
347 4
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298
329
401
456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C3H1-TYPE 1.
C3H1-TYPE 2.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 85.5; DB 1;
Pred. No. 0.0018;
8; Mismatches 23;
                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FF05B7D034C5EA9F CRC64;
                                                                                                                                                                                                                                                                               Hominidae; Homo
    BILAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 544;
                                                                                                                                                                                                                                                                                                                                                          (RAPSYN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                      the RAPSN gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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Best Local S
Matches 15
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InterPro; IPR001841; Znf_ring.
Pfam; PF00515; TPR; 5
PRINTS; PR00217; POSTSYNAPTIC.
ProDom; PD012428; POSTSYNAPTIC; 1
SMART; SM00184; RING; 1.
SMART; SM00028; TPR; 5.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-88246464; PubMed-3380101;

Takahashi M., Inaguma Y., Hiai H., Hirose F.;

Takahashi M., Inaguma Y., Hiai H., Hirose F.;

"Developmentally regulated expression of a human 'fi
"Developmentally regul
                                                                     gene encoded by the 5' half of the ret transformin Mol. Cell. Biol. 8:1853-1856(1988).
-!- FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVEL.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- DISEASE: RECOMBINATION OF THE N-TERMINAL OF RETYROSINE KINASE PRODUCES THE RET TRANSFORMING.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 BOX-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Zinc-finger protein RFP (Ret finger protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
ZN_FING
LIPID
                         This SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00405; 43_KD_POSTSYNAPTIC; PROSITE; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFP_HUMAN P14373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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362 402
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195 P
404 P
46199 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Postsynaptic TPR.
is copyright. It is produced through a collaboration stitute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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Pred. No. 0.00
10; Mismatches
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PHOSPHORYLATION (POTENTIAL)
6A9FBA4B95E58CBC CRC64;
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RING-TYPE.
MYRISTATE (BY SIMILARITY).
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a human 'finger'-containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS_MOUSE STANDARD; PRT;
P12672;
01-OCT-1989 (Rel. 12, Created)
01-AUG-1990 (Rel. 15, Last sequence to 16-OCT-2001 (Rel. 40, Last annotation 43 kba receptor-associated protein of the control of the cont
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InterPro: IPR003878; SPRY_domain
InterPro: IPR00315; Znf_bbox.
InterPro: IPR001841; Znf_ring.
Pfam; PF00643; Zf-B_box; 1.
Pfam; PF00643; Zf-B_box; 1.
Pfam; PF00097; Zf-G3HC4; 1.
                                                                                                                                                                                                                                                                                                                           OStoj...
RAPSN.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZN_FING
ZN_FING
DOMAIN
SEQUENCE
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SMART; SM00336; BBOX; 1.
SMART; SM00134; RING; 1.
SMART; SM001449; SPRY; 1.
PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS50119; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Proto-oncogene; Zinc-finger; Metal-binding; Chromosomal translocation; Nuclear protein; DNA-binding.
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MEDIINE-89008468; PubMed-3170600;
Frail D.E., McLaughlin L.L., Mudd J., Merlie J.P.;
"Identification of the mouse muscle 43,000-dalton
receptor-associated protein (RAPsyn) by cDNA cloni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                  "Experession of RNA transcripts for the innervated and denervated rat skeletal FEBS Lett. 249:229-233(1989).
                                                                                                                                                                                                                                    MEDLINE=89289985; PubMed=2737281;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Muscle;
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; A28101; TVHURF
; 602165; -
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an email to license@isb-sib.ch).
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t annotation update
d protein of the sy
ssociated 43 kDa pr
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RING-TYPE.
B BOX-TYPE.
SPRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 84; DB Pred. No. 0.008; Mismatches
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                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; | Sciurognathi; Muridae;
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the synapse (RAPSYN)
kDa protein) (43 kDa
                                                                                                                                                                      postsynaptic 43
muscle.";
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RESULT 13
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ID YQ57_C
AC Q09463
DT 01-NOV
DT 16-OCT
DE HYPOTH
GN C16C10
OS CAENOT
OC Rhabdi
OX NCBLT
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RP SEQUEN
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-i- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING THE NICOTINIC ACETYLCHOLINE RECEPTOR TO SYNAPTIC SITES. IT MAY LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON, POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
                                                                                                                                                                                          01-NOV-1997 (
01-NOV-1997 (
16-OCT-2001 (
Hypothetical
                                                                                                                                                                                                                                                                                         YQ57_CAEEL
Q09463;
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SEQUENCE
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SMART; SM00184; RING; 1.
SMART; SM00028; TPR; 3.
PROSITE; PS00405; 43_KD_POSTSYNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:99422; Rapsn.
InterPro; IPR001237; Postsynaptic
InterPro; IPR001440; TPR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00515; TPR; 6.
PRINTS; PR00217; POSTSYNAPTIC.
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-i- SIMILARITY: BELONGS TO THE RAPSYN FAMILY.
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
LIPID
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                                                                                                 Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00405; 43_KD_POSTSYNAPTIC; PROSITE; PS00518; ZF_RING_1; FALSE_NE PROSITE; PS50089; ZF_RING_2; 1.
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    SEQUENCE FROM N.A. STRAIN-BRISTOL N2
                                                                        NCBI_TaxID=6239;
                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                         C16C10.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                       362 CGLCGESIGERNSRLQALPCSHIFHLRCL----QNNGTRSCPNCR 402
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A31995; A31995.
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J03962; AAA40030.1;
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                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                             35,
40,
kDa
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                                                                                                 Nematoda; Chromadorea; inae; Caenorhabditis.
                                                                                                                                                                                          Last sequence update)
Last annotation update)
protein C16C10.7 in chromosome
                                                                                                                                                                                                                                                                  Created)
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MYRISTATE.

PHOSPHORYLATION (POTENTIAL PHOSPHORYLATION (POTENTIAL DV -> EL (IN REF. 2).

DV -> EL (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83.5; DB 1
Pred. No. 0.0025;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoskeleton; Phosphorylation;
                                                                                                                                                                                                                                                                                                                  235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                         Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
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Best Local
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  entities
or send a
                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way the state of the sta
                                                                                                                                                                                                                                                                                                                                   "The Drosophila melanogaster developmental gene zinc-finger-motif protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goliath protein (G1 protein).
GOL OR G1 OR GL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein;
ZN_FING 26 6
DOMAIN 121 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000306; Znf_FYVE.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                              between
                                                                                                                                                                                                                         ---
                                                                                                                                                                                                                                                                                                                                                                               Bouchard M.L., Cote
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93216124; PubMed=8462875;
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q06003;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOLI_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00064; FYVE; 1
SMART; SM00184; RING; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z46787; CAA86745.1; -. WormPep; C16C10.7; CE01498.
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Submitted (NOV-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAP-SRTCPQCR 47
                                                                                                                                                                                                                      PUTATIVE ROLE AS TRANSCRIPTION FACTOR. SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: VISCERAL MESODERM
                                                                                                                                                                             SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                       FUNCTION: REGULATION OF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS
                                                                                                                                                                                                    MUSCULATURE.
                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNIC---LDAAKDAVVSLCGHLFCWPCLSQWLDTRPNNQVCPVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                       requires a
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PS50089; ZF_RING_2;
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235 A
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124 F
172 F
24915 MW;
                    tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.0%;
37.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
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1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
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Pred. No. 0.00
6; Mismatches
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POLY-ALA.
; 21A04AE951F6382A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                         MESODERM AND
                                                                                                                                                                                                                                                                                         EXPRESSION DURING MESODERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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.0017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                         PRIMORDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 235;
                                                                                                       and the
                                                                                                                                                                                                                                                                                                                                                        gl encodes
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                                                                                                              EMBL
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                                                                                                            a collaboration
                                                                                                                                                                                                                                                                                                                                                        a variant
                                                                                                                                                                                                                         SOMATIC
                                                                                                                                                                                                                                                                                         FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
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Best Local S
Matches 16
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
PROSITE: PS0089; ZF_RING_2; 1.
Developmental protein; Zinc-finger; Transcription regulation; DNA-binding; Nuclear protein.
ZN_FING 126 167 RING-TYPE.
ZN_FING 126 259 GLN/PRO/SER-RICH.
DOMAIN 208 259 GLN/PRO/SER-RICH.
SEQUENCE 284 AA; 31973 MW; ECEE2D5EEDBALE2B CRC64;
                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ENthe European Bioinformatics Institute. There are no restructed the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-91249381; van Lohuiizen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-91249382; PubMed-1904009;
MICHARD W.S., Barri G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel.
01-MAY-1992 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                              -!- DISEASE: COOPERATES WITH THE MYC ONCOGENE TO -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                            by provirus tagging.";
Cell 65:737-752(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                        Haupt Y., Alexander W.S., Barri G., Klinken S.P., Adams J.M.; "Novel zinc finger gene implicated as myc collaborator by retrovirally accelerated lymphomagenesis in E mu-myc transgen
                                                                                                                                                                                                                                                                                                       "Identification of cooperating oncogenes in
                                                                                                                                                                                                                                                                                                                        Gulden H., Berns A.;
                                                                                                                                                                                                                                                                                                                                                                                              Cell 65:753-761(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BMI1 OR BMI-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polycomb complex protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 CAICIEAYKPTDTIRILPCKHEFHKNCIDPWLIE-----HRTCPMCKLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: DETECTED IN MOST ORGALEVELS IN THYMUS, HEART, BRAIN AND TESTIS
                                                                                                                                                                                                                                 FUNCTION: INVOLVED IN MAINTAINING STATE OF GENES. MODIFIES CHROMATIN IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                   SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED
                                                                                                                                                                                                         (PCG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTICSDFFDHSRDVAAMDCGHTFHLQC----LIQSFETAPSRTCPQCRIQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                    Verbbeek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22, Created)
22, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                    PubMed=1904008;
Verbbeek S., Scheijen B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.7%;
31.4%;
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Pred. No. 0.00
8; Mismatches
                                                                                                                                                                                                                                                CHROMATIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                         IN MOST ORGANS WITH HIGH EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324
                                                                                                                                                                                                                                                THE TRANSCRIPTIONALLY REPRESSIVE N, RENDERING IT HERITABLY CHANGED
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0.0027;
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                                                                                                                                                                                                                                                                                                         E mu-myc transgenic mice
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                                                                                                                                            PRODUCE
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                                                                                     EMBL
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                                                                                        a collaboration
MBL outstation -
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                                                                                     outstation
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BMI1_HUMAN STANDARE
P35226; Q96E37;
O1-FEB-1994 (Rel. 28, C
O1-FEB-1994 (Rel. 28, I
O1-MAR-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
SEQUENCE
                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Erythrocyte;
MEDLINE-94093545; PubMed-8268912;
Alkema M.J., Wiegand J., Raap A.K.,
"Characterization and chromosomal 1
                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Chromatin regulator; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oncogene
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ZN_FING 18 57 RING-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE
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                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear.
DISEASE: COOPERATES WITH THE MYC ONCOGENE TO SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                            IN ITS EXPRESSIBILITY.
SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED
                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no way to be a superior of the state of the st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCVLCGGYFIDATTI--IECLHSFCKTCIVRYLET--SKYCPICDVQV
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                          L13689;
    BC011652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.7%;
l Similarity 31.2%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          994 (Rel. 28, Last sequence up 002 (Rel. 41, Last annotation complex protein BMI-1.
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324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                          AAA19873.1;
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  AAH11652.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2:1597-1603(1993).
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324 P
36707 MW;
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Primates;
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Pred. No. 0.00
L3; Mismatches
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NUCLEAR LOCALIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription
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the human pr
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MIN; 164851,
InterPro; IPR001841; 2..._

R Pfam; PF00097; zf-C3HC4; 1.

R SMART; SM00184; RIGG; 1.

DR PROSITE; PS0089; ZF_RING_1; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

Chromatin regulator; Nuclear protein; Transcription regenerates of the protein of the prot
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ME18_MOUSE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAV-1992 (Rel. 22, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
DNA-binding protein Mel-18.
ZNF144 OR ZFP144 OR ZFP-144 OR MEL18 OR MEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                  Kanno M., Hasegawa M., Ishida A., Isono K., Taniguchi M.;
"mel-18, a Polycomb group-related mammalian gene, encodes a
transcriptional negative regulator with tumor suppressive activity.
EMBO J. 14:5672-5678(1995).
1- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS SPECIFICALLY TO THE
DNA SEQUENCE 5'GACTNGACT-3'. HAS A TUMOR SUPPRESSOR ACTIVITY.
MAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91060627; PubMed=2246278; Tagawa M., Sakamoto T., Shigemoto K., Ma Ito T., Nakamura I., Okitsu A., Imai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel.
01-MAY-1992 (Rel.
01-MAR-2002 (Rel.
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P23798;
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in various tumor cell
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                                                                                                                     DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED. DISEASE: PROBABLY RELATED TO TUMORGENESIS SINCE STRONGLY IN MOST TUMOR CELL LINES. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear TISSUE SPECIFICITY: EXPRESSED IN NEURAL TISSUES.
                                                                                                                                                                                                                                                                             CELL DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCVLCGGYFIDATTI--IECLHSFCKTCIVRYLET--SKYCPICDVQV
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15; Conserv
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81
251
265
326 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265:20021-20026(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovel DNA-binding protein with zinc
cells.";
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22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=8521824;
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326 P
265 V
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31.2%;
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Pred.
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0.0031;
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Best Local
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          between
the Euro
                                                                                                                 Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS SPECIFICALLY TO THE DNA SEQUENCE 5'GACTNGACT-3'. HAS A TUMOR SUPPRESSOR ACTIVITY. MAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEURAL
                                                                                                                                                                                                              Gene
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ME18_F
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or send an
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ZNF144 OR MEL18
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01-FEB-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                           TISSUE-Placenta;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                             Taniguchi M., Kanno M.;
"Cloning and chromosome mapping encodes a DNA-binding protein w. Gene 129:249-255(1993).
                                                                                                                                                                                                                                                       Ishida A., Asano H.,
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-93314969;
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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16-OCT-2001
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D90085; BAA14122.1; -. EMBL; BC016419; AAH16419.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
                                                  SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: DETECTED IN ALL TISSUE EX
EXPRESSION FOUND IN PLACENTA LUNG AND KIDNEY
IN LIVER, PANCREAS AND SKELETAL MUSCLE.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
            European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                               HOMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCALCGGYFIDATTI--VECLHSFCKTCIVRYLET--NKYCPMCDVQV
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18
81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00518; ZF_RING_1; 1.
PS50089; ZF_RING_2; 1.
Ption regulation; Repressor; Zinc-finger; DNA-binding;
                                                                                                              DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 AA;
                                                                                                                                                                                                                                                                                                                                                                   (Rel.
                                                                                                                                                                                                                                                                                                                                                        protein Mel-18
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                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Phosphorylation.
57 RING-
95 NUCLI
342 PRO/5
237 PHOSE
                                                                                                                                                                                                                                                                                                                                                                   28,
40,
                                                                                                                                                                                                                                                      PubMed=8325509;
H., Hasegawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          license agreement (See http://www.isb-sib.ch/announce/
license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.7%;
29.2%;
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                                                                                                                                                                                                                                                                                                                                                                  sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                        (Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82; DB
Pred. No. 0.00
L4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
C23031B8B9E30108 CRC64;
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PHOSPHORYLATION (BY CAPK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY CAPK)
                                                                                                                                                                                                                       with
                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                    of.
                                                                                                                                                                                                                       the hu
                                                                                                                                                                                                                                                       Koseki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
No.
long
                                                                                                                                                                                                                                                                                                                                                                                                              344
                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
0.0032;
                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                   RING-finger' mc',
                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                       Ono
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                                                                                       EXAMINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342;
                                                                                                                                                                                                                                                                                                                                                       144).
                                                                            AND
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 content
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                                                                            MOT
                                                                                                                                                                                                                                                      Yoshida M.C
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motif.";
                                                                                       HTTW
                                                                           EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local S
Matches 14
                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                        escapes X chromosome inactivation.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKR4_HU
Q13434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
SEQUENCE
                                                                                          InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF00642; zf-CCCH; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Makorin 4 (Zinc_finger protein 127-Xp) (ZNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001841; Znf. Pfam; PF00097; zf-C3HC4; SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKRN4 OR ZNF127L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 600346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D13969; BAA03074.1; -. EMBL; BC004858; AAH04858.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                       InterPro; IPR000571; InterPro; IPR001841;
                                                                                                                                                     EMBL; U41315; AAA99070.1; -.
                                                                                                                                                                                                                                                                                                                                                      "An X-linked
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Hendrich B.D., Longstreet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear
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18
81
242
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14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344
                                                                                                                                                                                                                                                                                                                                                    homologue of the autosomal imprinted gene ZNF127
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37788
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95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB Pred. No. 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION SIGNAL PRO/SER-RICH.
, A910BCD4C0CE9927 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                  Gustashaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82; DB 1;
No. 0.0032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485
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) (2NF127-Xp).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 344
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SMART; SM00184; RING; 1.
SMART; SM00356; ZnF\_C3H1; 4.
PROSITE; PS00518; ZF\_RING\_1;
PROSITE; PS50089; ZF\_RING\_2;

Zinc-finger;

Repeat. 96 1: 125 1:

C3H1-TYPE

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RESULT 21
Z173_HUMAN
ID Z173_H
AC Q12899
DT 16-OCT
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YP99_CA
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                                                                                                                                            Query Match
Best Local Similarity
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16-OCT-2001 (Rel. 40
Hypothetical 22.7 kD
C28H8.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Q09477;
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DOMAIN
ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                       InterPro; IPR001965; PHD.
InterPro; IPR001961; 2.
Pfam; PF00628; PHD; 2.
SMART; SM00249; PHD; 2.
SMART; SM00249; PHD; 2.
Hypothetical protein; 2inc-finger; Nuclear prote
EN_FING 86 142 PHD-TYPE 1.
EN_FING 143 191 PHD-TYPE 2.
SEQUENCE 202 AA; 22725 MW; F627355EB73AD26A
 Z173_HUMAN STANDARD;
Q12899;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                Miller N., Waterston R.;
Submilted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- SIMILARITY: BELONGS TO THE REQUIEM/D4 FAMILY.
-i- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                  WormPep; C28H8.9; CE06896.
                                                                                                                                                                                                                                                                                                              EMBL; U20861; AAA62297.1; -.
                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
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                                                                                   144
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                                                                                                         4
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                                                                                                 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAP--SRTCPQCRIQVG
                                                                                   CTICGTSENDDKLLFCDDCDRGYHLYCLTPALEKAPDDEYSCRLCQVEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCGICMEVVYEKANPNEHRFGILS-NCNHTFCLKCIRKWRSAKEFESRIVKSCPQCRI
                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 31.(
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
271
316
405
485
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peloderinae;
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298
370
425
52909 .
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40,
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0, Last annotation update
0, Tast annotation update
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                                                                                                                                          28.3%;
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MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
C3H1-TYPE 4.
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Pred. No. 0.00
12; Mismatches
                                                                                                                               9
                                                                                                                               Score 81; DB Pred. No. 0.00 9; Mismatches
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No. 0.0052;
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                        539
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in chromosome
                                                                                                                                          DB 1;
.0026;
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                                                                                                                                23;
                                                                                                                                                      Length 202;
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RESULT 22
2147_MOUSE
ID 2147_MOUSE
AC Q61510;
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Best Loc
Matches
                                                                                                                                                                                                                 PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS00518; ZF_RING_1; F)
PROSITE; PS00089; ZF_RING_2; 1
Zinc-finger; Coiled coil.
ZN_FING 16 57 R
ZN_FING 97 138 B
DOMAIN 188 227 C
DOMAIN 365 539 S
DOMAIN 388 400 P
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003877; InterPro; IPR003878; InterPro; IPR00315; InterPro; IPR001841;
                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE-96079113; PubMed-8530076;
Chu T.W., Capossela A., Coleman R.,
"Cloning of a new 'finger' protein (
region of the human MHC.";
Genomics 29:229-239(1995).
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3HC4; 1.
PRINTS; PR01406; BBOXZNFINGER
SMART; SM00336; BBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2.229,817bp genomic DNA of 6p21.3 HLA class submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat zinc finger protein 173 (Acid finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U09825; AAA93131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                           16
                                                                                                                                         Local
                                                                                                   4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSR-TCPQCR 47
                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600830;
                                                                           CSICLDYL---RDPVTIDCGHVFCRSCTTDVRPISGSRPVCPLCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP000517; BAB63330.1;
                                                                                                                                                                                                                                                                                                                                       SM00184; RING;
SM00449; SPRY;
                                                                                                                              17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001870;
                                                                                                                                                                                              422
539
                                                                                                                              Conservative
                                                                                                                                                                                              AA;
             STANDARD;
                                                                                                                                                                                            432 I
62165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                            Znf_bbox.
Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gamma_carbxylse.
                                                                                                                                         28.3%;
37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPRY_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leman R., Goei V.L., Nallur G., Gi
protein gene (ZNF173) within the
                                                                                                                             5.
                                                                                                                            Score 81; DB Pred. No. 0.005; Mismatches
                                                                                                                                                                                                                     B BOX-TYPE.
COILED COIL
SPRY.
POLY-GLU.
                                                                                                                                                                                            POLY-GLU.
842A71C41F2E2348 CRC64;
                                                                                                                                                                                                                                                                                                              FALSE_NEG
                                                                                                                                                                                                                                                                         RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein)
             634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                       DВ
                                                                                                                                         .0067;
             B
                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo
                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AFP)
                                                                                                                                                    Length 539;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yh a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gruen
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                                                                                                                              4.
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                                                                                                                              Gaps
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CBL_HCM_N
ID CBL_HCM_N
ID CBL_HCM_N
AC P2268
DT 01-AU
DT 16-OC
DE Signa
GN CBL_O
OS HOMO
OC EUKar
OC Mamma
OC NCBI
RN [1]
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RP SEQUE
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003877; SPRY.
InterPro; IPR003878; SPRY.domain.
InterPro; IPR001841; Znf_ring.
InterPro; IPR001841; Znf_ring.
Pfam; PF00622; SPRY; 1.
Pfam; PF00097; zf-C3HC4; 1.
SWART; SW00184; RING; 1.
SWART; SW00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS000518; ZF_RING_1; 1
PROSITE: PS50089; ZF_RING_2; 1
Zinc-finger; Coiled coil.
ZN_FING 13 54
DOMAIN 215 305 C
DOMAIN 514 631 S
SEQUENCE 634 AA; 71772 MW;
                                                                                                                                                                                          CBL_HUMAN STANDARD;
P22681;
O1-AUG-1991 (Rel. 19, Created)
O1-AUG-1991 (Rel. 19, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the profit institutions as long as its content use the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA in target organs.";
J. Biol. Chem. 270:24406-24413(1995).
-i- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-i- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                                                                                               Signal transduction CBL OR CBL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Zinc finger protein 147 (Estrogen responsive finger protein) (Efp).
ZNF147 OR ZFP147 OR EFP.
                                                                       Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orimo A., Inoue S., Ikeda K., Noji S., Muramatsu M.;
"Molecular cloning, structure, and expression of mouse estrogen-
responsive finger protein Efp. Co-localization with estrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Uterus, Ovary, and Placenta; MEDLINE-96025835; PubMed-7592654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001870; Gamma_carbxylse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFET-APSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                         CSVCLELF - - - KEPVTTPCGHNFCTSCLDETWVVQGPPYRCPQCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D63902; BAA09941.1; -. MGI:102749; Zfp147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity 33.: 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zfp147
                                                                       Chordata;
Primates;
                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.3%;
33.3%;
                                                                                                                                                                                               Last sequence up
                                                                                                                                                                   CBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81; DB
Pred. No. 0.00
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPRY.
; 6695C9DE2832E611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RING-TYPE.
COILED COIL (POTENTIAL).
                                                                  Craniata; Vertebrata; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                      (Proto-oncogene
                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                              906
                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
.0078;
                                                                                                                                                                                                                                                                                           A
                                                                       Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 634;
                                                                                                                                                                      c-CBL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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RESULT 24
YOUD\_CAEEL

P30631;

YOUD\_CAEEL

STANDARD;

PRT;

161

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В
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                                                                                                                                                                                                                                    SOFT TO THE TOWN REPRESENTATION OF THE TOWN REPR
                                                                                                  Matches
                                                                                                                             Query Match
Best Local
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Pfam; PF02262; Cbl_N; 1.

Pfam; PF02761; Cbl_N2; 1.

Pfam; PF002762; Cbl_N3; 1.

Pfam; PF00627; UBA; 1.

Pfam; PF00097; zf-C3HC4; 1.

SMART; SM00184; RING; 1.

SMART; SM00184; RING; 1.

PROSITE; PS00518; ZF_RING_1; 1.

PROSITE; PS00509; ZF_RING_2; 1.
                                                                                                                                                                                                                                  DOMAIN
DOMAIN
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 47-350.

**MEDLINE-99176421: pubmed=10078535;

Meng W., Sawasdikosol S., Burakoff S.J., Eck M.J.;

**Structure of the amino-terminal domain of Cbl complexed to its binding site on ZAP-70 kinase.";

*nature 398.84-90(1999).

-i- FUNCTION: PARTICIPATES IN SIGNAL TRANSDUCTION IN HEMATOPOIETIC CELLS. ADAPTOR PROTEIN THAT FUNCTIONS AS A NEGATIVE REGULATOR CHANNY SIGNALLING PATHWAYS THAT START FROM RECEPTORS AT THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91232862; PubMed=2030914;
Blake T.J., Shapiro M., Worse H.C. III, Langdon W.Y.;
"The sequences of the human and mouse c-cbl proto-oncogenes show v-cbl was generated by a large truncation encompassing a proline-rich domain and a leucine zipper-like motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proto-oncogene; Nuclear protein; Zinc-finger; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003153; Cbl_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 1 RING-TYPE Z
-!- SIMILARITY: CONTAINS 1 UBA DOMAIN.
380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000449; UBA.
                                              3 LCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: PHOSPHORYLATED ON TYROSINE
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LCKICA---ENDKDVKIEPCGHLMCTSCL-TSWQESEGQGCPFCRCEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A43817; A43817.
1B47; 27-APR-99.
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                                                                                                    16;
                                                                                                                             Similarity
                                                                                                                                                                                                                                       906
                                                                                                    Conservative
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                                                                                                                                                                                                                                                          127
420
476
688
688
834
895
700
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                                                                                                                             28.0%;
33.3%;
                                                                                                                                                                                                                                       X.
                                                                                                  10;
                                                                                                                             Score 80; DB 1;
Pred. No. 0.015;
                                                                                                                                                                                                                                  PHOSPHORYLATION.
7D686B050204AD8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                 ASP/GLU-RICH PRO-RICH.
                                                                                                                                                                                                                                                                                        PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                              ASP/GLU-RICH
UBA.
                                                                                                                                                                                                                                                                                                                                                                                                                        RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC
                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                         (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                             (ACIDIC).
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                                                                                                    18;
                                                                                                                                                     Length 906
                                                                                                  Indels
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                                                                                                  Gaps
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RESULT
2179_HU
ID 2179_HU
AC QS
DT 11
DT 11
DT 2
OS F
OC F
OC F
OX F
OX F
OX F
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Best Local
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16-OCT-2001 (Rel. 4
Hypothetical 18.8 kt
ZK637.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZK63/.14.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                         O9ULX5; O60633;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update
Zinc finger protein 179 (Brain finger protein 20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2:
MEDLING-92168156; PubMed-1538779;
Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Coulson
Craxton M., Durbin R.K., Berks M., Metzstein M., Hawkins T.,
Ainscough R., Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001841; Znf_ring.
pfam; pF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; pS00518; ZF_RING_1; FALSE_NEG
PROSITE; PS0089; ZF_RING_2; 1.
                                                                                                                                                                                                                 HUMAN
Z179_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Zinc-finger.
ZN_FING 72 134 RING-
SEQUENCE 161 AA; 18847 MW; F5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z11115; CAA77447.1; -. PIR; S15788; S15788. WormPep; ZK637.14; CE00432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The C. elegans genome sequencing project: a beginning."; Nature 356:37-41(1992).
                SEQUENCE FROM N.A.
Seki N., Hattori A.,
"Human BFP/ZNF179.";
                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                       NCBI_TaxID=9606
                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                        128
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                                                                                                                                                                                                                                                                                        QTCPTCRQKV 137
                                                                                                                                                                                                                                                                                                                 RTCPQCRIQV 50
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                 STANDARD;
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27,
40,
kDa
                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                   27.8%;
30.0%;
  to the EMBL/GenBank/DDBJ databases
                             Saito
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Last annotation update)
protein ZK637.14 in chromosome
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Last
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                               T.;
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 79.5; DB 1;
Pred. No. 0.0032;
4; Mismatches 22;
                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                 PRT;
                                                                                                                                         update)
                                                                                                                                                                                                                 632 AA
                                                                                                                                                                                                                                                                                                                                                                        -- VAAMDCGHTFHLQCLIQSFETAPS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FINGER.
                                                                                      Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                 P46580;
01-NOV-1995
01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 146.8 kDa protein C34E10.5 in chromosome
C34E10.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZN_FING
SEQUENCE
                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RNCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1;
PROSITE; PS50089; ZF_RING_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               finger protein (bfp), a me Genomics 33:325-327(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuda Y., Inoue S., Seki N., Ho
                                                                                                                                                            -i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-i- SIMILARITY: TO S.POMBE SKB1 AND YEAST YBR133C
                                                                                                                                                                                                                   Kirsten
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB026054; EMBL; AF054587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Predominantly expressed
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE OF 33-127 FROM N.A.
         Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         YLB5_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc-finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Chromosome mapping of human (2NF179), mouse, and finger protein (bfp), a member of the RING finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 CSIC---LERLRDPISLDCGHDFCIRC----FSTHRLPGCEPPCCPECR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFET----APSRTCPQCR
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17; Conser
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632 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAA84698.1; -. AAC08584.1; -.
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68354 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.6%;
34.7%;
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Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 632;
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Best Local
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                                                                                                                        InterPro; IPR003877; SPRY_domain.
InterPro; IPR003878; SPRY_domain.
InterPro; IPR00315; Znf_bbox.
InterPro; IPR000315; Znf_ring.
InterPro; IPR001841; Znf_ring.
Pfam; PF00622; SPRY; 1.
Pfam; PF00643; Zf-B_box; 1.
Pfam; PF00643; Zf-B_box; 1.
Pfam; PF000997; Zf-G3HC4; 1.
PRINTS; PR01406; BBOXZNFINGER.
SMART; SM00316; BBOX; 1.
SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
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PROSITE; PS00518; ZEF_R;

PROSITE; PS50089; ZEF_R;

PROSITE; PS50089; ZEF_R;

Hypothetical protein;

TRANSMEM 69 89

TRANSMEM 1165

ZN_FING 1222 1267
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01-NOV-1997
01-NOV-1997
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
PROSITE; PS50119; ZE_BBOX; 1.
PROSITE; PS50181; ZE_RING_1; 1.
PROSITE; PS50089; ZE_RING_2; 1.
Zinc-finger; Metal-binding; Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97176437; pubMed=9023983;
Cao T., Shannon M., Handel M.A., Etkin L.D.;
"Mouse ret finger protein (rfp) proto-oncogene
specific stages of mouse spermatcogenesis.";
Dev. Genet. 19:309-320(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:97904; Rfp. InterPro; IPR001870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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[1]
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER
SIMILARITY: CONTAINS 1 SPRY DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L46855; AAA85354.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00097; zf-C3HC4; 
; SM00184; RING; 1.
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00518; ZF_RING_1; PS50089; ZF_RING_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1281 AA;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Latement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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RESULT 28
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                                                                                                         SEQUENCE FNOT ....

STRAIN-S288C / AB972:

STRAIN-S288C / AB972:

Murphy L., Harris D., Barrell B.G., Rajandream M.A.;

Murphy L., Harris D., Barrell B.G., Rajandream M.A.;

Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

SUBMITTED THE PHEROMONE SIGNAL TRANSDUCTION PATHWAY.

IT MEDIATES PHEROMONE SIGNALS ACTING BETWEEN STE20 AND STEll.

IT IS ABSOLUTELY REQUIRED FOR PHEROMONE-INDUCED TRANSCRIPTION OF PHEROMONE STRAIN AND PLAY A ROLE IN CELL-CYCLE ARREST IN RESPONSE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STE5_YEAST
P32917;
01-OCT-1993
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ZN_FING
DOMAIN
SEQUENCE
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MEDLINE=93296161; PubMed=8516289;

Perlman R., Yablonski D., Simchen G., Levitzki A.;

Perlman R., Yablonski D., Simchen G., Levitzki A.;

"Cloning of the STE5 gene of Saccharomyces cerevisiae as a suppressor of the mating defect of cdc25 temperature-sensitive mutants.";

proc. Natl. Acad. Sci. U.S.A. 90:5474-5478(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE=93204951; PubMed=8455598;
Mukai Y., Harashima S., Oshima Y.;
"Function of the ste signal transduction pathw
pheromones sustains MAT alpha 1 transcription
cerevisiae.";
                     <del>:</del>
                                                                                                                                                                                                                                                                                                                                                               protein kinase
to Far1.";
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning
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STRAIN=DBY939;
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Mackay V.L., 1
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01-OCT-1996
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                                                         PHEROMONE.
SUBCELLULAR LOCATION: Cytopl
PTM: MAY BE REGULATED AT THE
MATING TYPE OF THE CELL AND
                   RESPONSE PAY
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8246877;
rd D., Harcus D.,
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                     YEAST
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                                                                                                       Cytoplasmic
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This SWI between the Euro

try is copyright. It is produced through a collaboration - Institute of Bioinformatics and the EMBL outstation -

There are no restrictions ng as its content is in

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Oncogene 10:2367-2377 (1995).
-!- SUBUNIT: INTERACTS WITH SH3 DOMAIN PROTEINS FYN,
-!- SUBCELULAR LOCATION: Nuclear (Potential).
-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM (SH
TRUNCATED ISOFORM 1 AND TRUNCATED ISOFORM 2; ARE
ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, KIDNEY, SI
AS WELL AS FETAL BRAIN AND LIVER AND HEMATOPOIETI
AS WELL AS FETAL BRAIN, LIVER, PANCREAS, SALIVARY GLA
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Best Local Similarity 30.4%;
Matches 17; Conservative
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_CBLB_HUMAN STANDARD; PRT; yoz c...
(13191; Q13192; Q13193;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Cast annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95303504; PubMed=7784085; Keane M.M., Rivero-Lezcano O.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                  between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keane M.M., Rivero-Lezcano Lipkowitz S.;
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BL; L01620; AAA35115.1; -.
BL; L12885; AAA35115.1; -.
BL; L07865; AAA16896.1; -.
BL; 247746; CAA87679.1; -.
BL; 39920; S39920.
CARP; S39920; S39920.
CARP; SM001841; Znf_ring.
ARP; SM00184; RING; 1.
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Wheen the Swiss Institute of Bioinformatics Institute. The European Bioinformatics Institutions as long the company of the c
                                                                                                                                                              PTM: PHOSPHORYLATED ON TYROSINES. SIMILARITY: CONTAINS 1 RING-TYPE Z SIMILARITY: CONTAINS 1 UBA DOMAIN.
                                   European
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                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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LG -> W (IN REF. 2).
NSI -> TLS (IN REF. 2).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
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long
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RESULT 30
MKR2_HUMAN
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Matches 15
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Pfam; PF02262; Cbl_N; 1.
Pfam; PF02761; Cbl_N2; 1.
Pfam; PF02762; Cbl_N3; 1.
Pfam; PF00627; UBA; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00185; UBA; 1.
SMART; SM00185; UBA; 1.
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SEQUENCE
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MEDLINE=21481893; PubMed=11597136;

MEDLINE=21481893; PubMed=11597136;

Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls

"Phylogenetic conservation of the makorin-2 gene, encoding

zinc-finger protein, antisense to the rafl proto-oncogene."

Genomics 77:119-126(2001).
                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                             MKR2_HUMAN STANDARD; PRT; 416 AA Q9H000; Q9NRY1; Q9BUY2; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat makerin 2 (HSPC070).
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U26710; AAB09291.1; -.
EMBL; U26711; AAB09292.1; -.
EMBL; U26712; AAB09293.1; -.
HSSP; P22681; 1B47.
MIM; 604491; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Some send an email to license@isb-sib.ch).
MEDLINE=20499367; PubMed=11042152; Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G. Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao J.-Zhang J.-Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.; Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.; Tcloning and functional analysis of cDNAs with open reading frames 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.";
                                                                                           SEQUENCE FROM N.A.
TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00518; ZF_RING_1; 1. PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000449;
InterPro; IPR001841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                               NCBI_TaxID=9606;
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l Similarity 31.2%;
l5; Conservative 1
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11; Mismatches
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MW; 038D4965DAFB98CB CRC64;
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InterPro; IPRO01841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF000642; zf-C3CH; 4.
SMART; SM00184; RING; 1.
SMART; SM001855; ZnF_C3H1; 4.
                                                                                             MKR2_MOUSE STANDARI
OPERVI; Q9DOL9;
01-MAR-2002 (Rel. 41, 0
01-MAR-2002 (Rel. 41, 1
01-MAR-2002 (Rel. 41, 1
                                                                                                                                                                                                                                                                                      Zinc-finger;
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ZN_FING
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ZN_FING
CONFLICT
CONFLICT
SEQUENCE
41
                                                                                                                                                   _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                          MKRN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome
   MEDLINE-21481893; PubMed-11597136
             SEQUENCE FROM N.A
                               NCBI_TaxID=10090;
                                                                                     Makorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                           VCSICMEVILEKASASERRFGILSNCNHTYCLSCIRQWRCAKQFENPIIKSCPECRV
                                                                                                                                                                                                                LCTICSDFF-----DHSRDVAAMDCGHTFHLQCLIQ-----SFETAPSRTCPQCRI
                                                                                                                                                                                                                                      l Similarity
16; Conser
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PS00518; ZF_RING_1;
PS50089; ZF_RING_2;
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annotation update)
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
MAKORIN-TYPE 4.
C3H1-TYPE 4.
F -> V (IN REF. 2 AND 3).
K -> E (IN REF. 2).
W; 02B6B7A8BD38ZDDC CRC64;
                                                                                                                                                                                                                                   Score 76.5; Di
Pred. No. 0.01
10; Mismatches
                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 32
TTC3_HUMAN
ID TTC3_HUMAN
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Mynshaw. Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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MGD; MGI:1914277; Mkrn2.

InterPro; IPR000571; Zf-CCH.

InterPro; IPR001841; Znf_ring.

Pfam; PF00097; Zf-C3HC4; 1.

Pfam; PF000642; Zf-CCCH; 4.

SMARR; SM00184; RING; 1.

SMARR; SM00356; ZF-RING_1; 1.

PROSITE; PS00518; ZF_RING_1; 1.

PROSITE; PS0089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
ZN_FING
CONFLICT
SEQUENCE
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ZN_FING
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA Nature 409:685-690(2001).
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.; "Phylogenetic conservation of the makorin-2 gene, encoding a mulzino-finger protein, antisense to the rafl proto-oncogene."; Genomics 77:119-126(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger;
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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-!- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
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16; Conserv
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
L -> F (IN REF. 2).
LY-> F (SUR REF. 2).
MY: SF268E6B9D9A6C9F CRC64;
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Pred. No. 0.01
10; Mismatches
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Metazoa; Chordata;
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Tetratricopeptide repeat protein 3 (TPR repeat
                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                     REPEAT
ZN_FING
                                                                                                                                                                                                                                                                                                      SMART; SM00184; RING; 1.
SMART; SM00028; TPR; 3.
PROSITE; PS00518; ZF_RING_1;
PROSITE; PS50089; ZF_RING_2;
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00515; TPR; 4.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsukahara F., Hattori M., Muraki T., Sakaki Y.;
"Identification and cloning of a novel cDNA belonging to
tetratricopeptide repeat gene family from Down syndrome-critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome
DNA Res. 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96281123;
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Mammalia; Eutheria;
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InterPro; IPR001841; Znf_ring.
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EMBL; D84294;
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Tsukahara F., Hatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of a novel human gene containing the tetratricopeptide repeat domain from the Down syndrome region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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01-OCT-1996
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SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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D84296;
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ma A., Suzuki E.,
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ARG/LYS-RICH (BASIC).

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                                                                                                                                                                                   TPR 3.
TPR 4.
RING-TYPE.
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POLY-LYS.
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                                                                                                                                                                                                                                                                                        Alternative
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Best Local
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                                                                                                Pfam; PR00622; SPRY; 1.
Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3Hc4; 1.
PRINTS; PR01406; BBOXZNFINGER.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
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15-JUL-1998 (Rel.
16-OCT-2001 (Rel.
                                                                PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-Macrophage;
MEDLINE-96215393; PubMed-8625517;
Keech C.L., Gordon T.P., McCluskey J.;
"Structural differences between the hu
autoantigens associated with poorly co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RO52)
SSA1 C
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                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
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                                            ZN_FING
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InterPro; IPR001841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 BOX-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 SPRY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                    n. Exp. Immunol. 104:255-263(1996).
FUNCTION: RO/SSA IS A RIBONUCLEOPROTEIN PARTICLE COMPOSED SINGLE POLYPEPTIDE AND ONE OF FOUR SMALL RNA MOLECULES. IT PRESENT IN ALL MAMMALIAN CELLS STUDIED BUT HAS NO KNOWN FU
                                                                                                                                                                                                                                     MGI:106657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEICHEVF-KSKNVRVLKCGHKYHKGCFKQWLK--GQSACPACQ
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                                                             PS50119; ZF_BBOX; 1.
PS00518; ZF_RING_1; 1.
PS50089; ZF_RING_2; 1.
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IPR001870; Gamma_carbxylse.
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                     Antigen;
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Rodentia;
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34.1%;
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                                         RNA-binding; Ribonucleoprotein; RING-TYPE.
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syndrome type A antigen
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Pred. No. 0.12
7; Mismatches
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                      B BOX-TYPE.
LEUCINE-ZIPPER
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           393AE5AFD254855B CRC64;
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YQ55_CAEEL

Q09251;

Q1_NOV-1997 ()

Q1_NOV-1997 ()

16_OCT-2007 ()

Hypothetical

C16C10.5
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070418;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Zinc_finger_protein 179 (Brain finger
                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Ouchi Y., Muramatsu M.;
"A novel RING finger protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=98042506;
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Mammalia; Eutheria; Rodentia;
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      Rhabdītidae;
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
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TISSUE SPECIFICITY: Predominantly expressed i
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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16; Conserv
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                                                                                                                                                                                   STANDARD;
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kDa
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34.0%;
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Pred.
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                                                                                                                                                                                                                                                                                                              Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Diprotodontia; Macropodidae; N
NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Makorin
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                                                                          "The ancient source of a distinct gene famil
featuring RING and C(3)H zinc-finger motifs
in developing brain and nervous system.";
Genomics 66:76-86(2000).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20304755; PubMed=10843807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9TT91;
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                        -!- SIMILARITY:
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17; Conser
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MBL outstation -
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Q9QXP6;

01-MAR-2002

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SEQUENCE
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InterPro; IPR001395; Aldo_ket_red.
InterPro; IPR000571; zf-CCCH.
InterPro; IPR001841; znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF00642; zf-CCCH; 4.
                    EMBL;
                                                                                                                                                                           the
                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                           MEDLINE=20304755; PubMed=10843807; Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smith Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.; "The ancient source of a distinct gene family encoding profeaturing RING and C(3)H zinc-finger motifs with abundant in developing brain and nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER. SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
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                      ; AF192785; AAF17488.1; -. MGI:1859353; Mkrn1.
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; SM00356; ZnF_C3H1; 4.

!TE; PS00518; ZF_RING_1; 1

!TE; PS50089; ZF_RING_2; 1
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478 AA;
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Rodentia;
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28.1%;
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
C3H1-TYPE 4.
C3H1-TYPE 4.
CB2D9B147433853E CRC64;
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Matches 16
                                                                                                                        wiemann S., Well B., Wellenreuther R., Gassenhuber J., Glass
A Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
A Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubne
A Wambutt R., Korn B., Klein M., Poustka A.;
T "Towards a catalog of human genes and proteins: sequencing a
analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435(2001).
C -!- TISSUE SPECIFICITY: Ubiquitous.
C -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UHC7; Q9UEZ7; Q9H0G0;
01-MAR-2002 (Rel. 41, C
01-MAR-2002 (Rel. 41, L
01-MAR-2002 (Rel. 41, L
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SMART; SM00356; ZnF_C3H1; 4.
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                        use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; AF192784;
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MEDLINE=21154917; PubMed=11230166;
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16; Conservative
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281
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481 AA;
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 AAF17487.1;
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108 C
232 C
263 M
335 R
339 R
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Primates;
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k; Pred. No. 0.05
11; Mismatches
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C3H1-TYPE 2.
C3H1-TYPE 3.
MAKORIN-TYPE CYS-HIS.
RING-TYPE 4.
C3H1-TYPE 4.
C3H1-TYPE 4.
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                                                                                                                                                                                sequencing and uman cDNAs.";
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RESULT 39
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InterPro; IPR001841; znf_ring.
Pfam; PP00097; zf-C3HC4; 1.
Pfam; PF00642; zf-CCCH; 4.
Pfam; PF00642; zf-CCCH; 4.
SMART; SM00184; RING; 1.
SMART; SM00356; znF_C3H1; 4.
PROSITE; PS00518; zF_RING_1; 1.
PROSITE; PS00518; zF_RING_2; 1.
PROSITE; PS00518; zF_RING_2; 1.
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ZN_FING
VARIANT
                                                                                                                                                                                                                                                                               Nhan M., Rifkin L., Kil
Vignati D., Wilcox L.,
                                                                                                                                                                                                                                                                                                      Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
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                                                                                                                                                                                    Science 265:2077-2082(1994).
-!- SIMILARITY: TO C.ELEGANS EEED8.9
                                                                                                       between
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                                                                                                                                                                                                                                                 "Complete nucleotide sequence
                                                                                                                                                                                                                                                                      Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales;
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Eukaryota; Fungi; Ascomycota; Saccharomyc
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                                    s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outset European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for complete the statement is not removed.
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, AF192789; AAF18979.1;

, AF192790; AAF18979.1;

, AF192791; AAF18979.1;

, AF192792; AAF18979.1;

, AL136812; CAB66746.1;

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license agreement (See http://www.isb-sib.
license@isb-sib.ch).
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Best Local
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Interpro; IPR001841; Znf_ring.

Interpro; IPR001607; zf-UBP.

Pfam; PF00099; zf-C3HC4; 1.

Pfam; PF02148; zf-UBP; 1.

SMART; SM00184; RING; 1.

SMART; SM00290; ZnF_UBP; 1.

PROSITE; PS00518; ZF_RING_1; FALSE_PROSITE; PS00518; ZF_RING_2; 1.

Hypothetical protein; Zinc-finger.
ZN_FING 240 280 RING-T
SEQUENCE 585 AA; 67503 MW; 88FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9WTV7;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                    EMBL; AF069992; Ar
MGD; MGI:1342291;
                                                                                                                                                                       "RLIM inhibits functional activity of LIM homeofactors via recruitment of the histone deacety.
Nat. Genet. 22:34-399(1999).

"I- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR I
TRANSCRIPTION FACTORS. VIA THE RECRUITMENT
DEACETYLASE COREPRESSOR COMPLEX.

"I- SUBUNIT: ASSOCIATES WITH LIN/HOMEOBOX FACTOR!

"I- SUBUNIT: ASSOCIATES WITH LIN/HOMEOBOX FACTOR!

"I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGI
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RN12_MOUSE
                                                               modified and this statement is not removed
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                       MEDLINE=99364422; PubMed=10431247;
Bach I., Rodriguez-Esteban C., Carriere C.,
Rose D.W., Glass C.K., Andersen B., Izpisua
Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                        "Opposing developmental functions of positive coregulators of LIM homeodomain factors."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RING finger protein 12 (LIM domain interacting RI
(RING finger LIM domain-binding protein) (R-LIM).
RNF12 OR RLIM.
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PIR;
                                                                                                          the European Bioinformatics Institute. The By non-profit institutions as long
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                                      AF069992; AAD34209 1;
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6; Mismatches
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InterPro;

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